

WHAT IS CLAIMED IS:

1. A DNA encoding a protein selected from the group consisting of (A), (C), (E), (G), (I), (K), (M), (O), (Q), (S), (U), and (W), wherein said protein has an amino acid sequence defined as follows:

5 (A) an amino acid sequence consisting of amino acid residue numbers 23 to 616 of SEQ ID NO: 6,

(C) an amino acid sequence consisting of amino acid residue numbers 21 to 619 of SEQ ID NO: 12,

10 (E) an amino acid sequence consisting of amino acid residue numbers 23 to 625 of SEQ ID NO: 18,

(G) an amino acid sequence consisting of amino acid residue numbers 23 to 645 of SEQ ID NO: 23,

(I) an amino acid sequence consisting of amino acid residue numbers 26 to 620 of SEQ ID NO: 25,

15 (K) an amino acid sequence consisting of amino acid residue numbers 18 to 644 of SEQ ID NO: 27,

(M) an amino acid sequence consisting of SEQ ID NO: 6,

(O) an amino acid sequence consisting of SEQ ID NO: 12,

(Q) an amino acid sequence consisting of SEQ ID NO: 18,

20 (S) an amino acid sequence consisting of SEQ ID NO: 23,

(U) an amino acid sequence consisting of SEQ ID NO: 25, or

(W) an amino acid sequence consisting of SEQ ID NO: 27.

2. A recombinant DNA comprising the DNA according to Claim 1.

3. A transformed cell comprising the recombinant DNA according to

25 Claim 2.

4. A method for producing a peptide-forming enzyme comprising:
culturing the transformed cell according to Claim 3 in a medium for a
time and under conditions suitable to produce the peptide-forming enzyme,
and
5 accumulating the peptide-forming enzyme in the medium and/or
transformed cell.
5. A method for producing a dipeptide comprising:
culturing the transformed cell according to Claim 3 in a medium for a
time and under conditions suitable to produce a peptide-forming enzyme in a
10 culture, and
mixing the culture with a carboxy component and an amine
component to synthesize a dipeptide by enzymatic catalysis facilitated by a
peptide-forming enzyme encoded by said DNA.
6. The method for producing a dipeptide according to Claim 5,
15 wherein said cell is a microbe belonging to the genus *Sphingobacterium* that
has an ability to form the dipeptide from the carboxy component and the
amine component.
7. The method for producing a dipeptide according to Claim 6,
wherein said cell is separated from said culture.
- 20 8. The method for producing a dipeptide according to Claim 6,
wherein said cell is a treated microbial cell product of the microbe.
9. A DNA encoding a protein selected from the group consisting of
(B), (D), (F), (H), (J), (L), (N), (P), (R), (T), (V), and (X), wherein said protein
has an amino acid sequence defined as follows:
25 (B) an amino acid sequence including substitution, deletion,

- insertion, addition, and/or inversion of one or a plurality of amino acids in amino acid residue numbers 23 to 616 of SEQ ID NO: 6, and has at least 50% of the peptide-forming activity of a protein corresponding to unmutated amino acid residue numbers 23 to 616 of SEQ ID NO: 6 at 50°C and a pH of 8,
- (D) an amino acid sequence including substitution, deletion, insertion, addition, and/or inversion of one or a plurality of amino acids in amino acid residue numbers 21 to 619 of SEQ ID NO: 12, and has at least 50% of the peptide-forming activity of a protein corresponding to unmutated amino acid residue numbers 21 to 619 of SEQ ID NO: 12 at 50°C and a pH of 8,
- (F) an amino acid sequence including substitution, deletion, insertion, addition, and/or inversion of one or a plurality of amino acids in amino acid residue numbers 23 to 625 of SEQ ID NO: 18, and has at least 50% of the peptide-forming activity of a protein corresponding to unmutated amino acid residue numbers 23 to 625 of SEQ ID NO: 18 at 50°C and a pH of 8,
- (H) an amino acid sequence including substitution, deletion, insertion, addition, and/or inversion of one or a plurality of amino acids in amino acid residue numbers 23 to 645 of SEQ ID NO: 23, and has at least 50% of the peptide-forming activity of a protein corresponding to unmutated amino acid residue numbers 23 to 645 of SEQ ID NO: 23 at 50°C and a pH of 8,
- (J) an amino acid sequence including substitution, deletion, insertion, addition, and/or inversion of one or a plurality of amino

- acids in amino acid residue numbers 26 to 620 of SEQ ID NO: 25, and has at least 50% of the peptide-forming activity of a protein corresponding to unmutated amino acid residue numbers 26 to 620 of SEQ ID NO: 25 at 50°C and a pH of 8,
- 5 (L) an amino acid sequence including substitution, deletion, insertion, addition, and/or inversion of one or a plurality of amino acids in amino acid residue numbers 18 to 644 of SEQ ID NO: 27, and has at least 50% of the peptide-forming activity of a protein corresponding to unmutated amino acid residue numbers
- 10 18 to 644 of SEQ ID NO: 27 at 50°C and a pH of 8,
- (N) a mature protein region, having an amino acid sequence including substitution, deletion, insertion, addition, and/or inversion of one or a plurality of amino acids in an amino acid sequence consisting of SEQ ID NO: 6, and has at least 50% of
- 15 the peptide-forming activity of a protein corresponding to unmutated SEQ ID NO: 6 at 50°C and a pH of 8,
- (P) a mature protein region, having an amino acid sequence including substitution, deletion, insertion, addition, and/or inversion of one or a plurality of amino acids in an amino acid
- 20 sequence consisting of SEQ ID NO: 12, and has at least 50% of the peptide-forming activity of a protein corresponding to unmutated SEQ ID NO: 12 at 50°C and a pH of 8,
- (R) a mature protein region, having an amino acid sequence including substitution, deletion, insertion, addition, and/or
- 25 inversion of one or a plurality of amino acids in an amino acid

- sequence consisting of SEQ ID NO: 18, and has at least 50% of the peptide-forming activity of a protein corresponding to unmutated SEQ ID NO: 18 at 50°C and a pH of 8,
- (T) a mature protein region, having an amino acid sequence including substitution, deletion, insertion, addition, and/or inversion of one or a plurality of amino acids in an amino acid sequence consisting of SEQ ID NO: 23, and has at least 50% of the peptide-forming activity of a protein corresponding to unmutated SEQ ID NO: 23 at 50°C and a pH of 8,
- (V) a mature protein region, having an amino acid sequence including substitution, deletion, insertion, addition, and/or inversion of one or a plurality of amino acids in an amino acid sequence consisting of SEQ ID NO: 25, and has at least 50% of the peptide-forming activity of a protein corresponding to unmutated SEQ ID NO: 25 at 50°C and a pH of 8, or
- (X) a mature protein region, having an amino acid sequence including substitution, deletion, insertion, addition, and/or inversion of one or a plurality of amino acids in an amino acid sequence consisting of SEQ ID NO: 27, and has at least 50% of the peptide-forming activity of a protein corresponding to unmutated SEQ ID NO: 27 at 50°C and a pH of 8.
10. The DNA according to Claim 9, wherein said plurality is 2 to 50 amino acid residues.
11. A recombinant DNA comprising the DNA according to Claim 9.
12. A transformed cell comprising the recombinant DNA according to

Claim 11.

13. A method for producing a peptide-forming enzyme comprising:
culturing the transformed cell according to Claim 12 in a medium for a
time and under conditions suitable to produce the peptide-forming enzyme,
5 and
accumulating the peptide-forming enzyme in the medium and/or
transformed cell.

14. A method for producing a dipeptide comprising:
culturing the transformed cell according to Claim 12 in a medium for a
10 time and under conditions suitable to produce a peptide-forming enzyme in a
culture, and
mixing the culture with a carboxy component and an amine
component to synthesize a dipeptide by enzymatic catalysis facilitated by a
peptide-forming enzyme encoded by said DNA.

15 15. The method for producing a dipeptide according to Claim 14,
wherein said cell is a microbe belonging to the genus *Sphingobacterium* that
has an ability to form the dipeptide from the carboxy component and the
amine component.

16. The method for producing a dipeptide according to Claim 15,
20 wherein said cell is separated from said culture.

17. The method for producing a dipeptide according to Claim 15,
wherein said cell is a treated microbial cell product of the microbe.

18. A DNA selected from the group consisting of (a), (c), (e), (g), (i),
(k), (m), (o), (q), (s), (u), and (w), wherein said DNA has a base sequence
25 defined as follows:

- (a) a base sequence consisting of base numbers 127 to 1908 of SEQ ID NO: 5,
- (c) a base sequence consisting of base numbers 121 to 1917 of SEQ ID NO: 11,
- 5 (e) a base sequence consisting of base numbers 127 to 1935 of SEQ ID NO: 17,
- (g) a base sequence consisting of base numbers 127 to 1995 of SEQ ID NO: 22,
- (i) a base sequence consisting of base numbers 104 to 1888 of SEQ ID NO: 24,
- 10 (k) a base sequence consisting of base numbers 112 to 1992 of SEQ ID NO: 26,
- (m) a base sequence consisting of base numbers 61 to 1908 of SEQ ID NO: 5,
- 15 (o) a base sequence consisting of base numbers 61 to 1917 of SEQ ID NO: 11,
- (q) a base sequence consisting of base numbers 61 to 1935 of SEQ ID NO: 17,
- (s) a base sequence consisting of base numbers 61 to 1995 of SEQ ID NO: 22,
- 20 (u) a base sequence consisting of base numbers 29 to 1888 of SEQ ID NO: 24, or
- (w) a base sequence consisting of base numbers 61 to 1992 of SEQ ID NO: 26.
- 25 19. A recombinant DNA comprising the DNA according to Claim 18.

20. A transformed cell comprising the recombinant DNA according to Claim 19.

21. A method for producing a peptide-forming enzyme comprising:
culturing the transformed cell according to Claim 20 in a medium for a
5 time and under conditions suitable to produce the peptide-forming enzyme,
and
accumulating the peptide-forming enzyme in the medium and/or
transformed cell.

22. A method for producing a dipeptide comprising:
10 culturing the transformed cell according to Claim 20 in a medium for a
time and under conditions suitable to produce a peptide-forming enzyme in a
culture, and
mixing the culture with a carboxy component and an amine component
to synthesize a dipeptide by enzymatic catalysis facilitated by a
15 peptide-forming enzyme encoded by said DNA.

23. The method for producing a dipeptide according to Claim 22,
wherein said cell is a microbe belonging to the genus *Sphingobacterium* that
has an ability to form the dipeptide from the carboxy component and the
amine component.

20 24. The method for producing a dipeptide according to Claim 23,
wherein said cell is separated from said culture.

25. The method for producing a dipeptide according to Claim 23,
wherein said cell is a treated microbial cell product of the microbe.

26. A DNA selected from the group consisting of (b), (d), (f), (h), (j), (l),
25 (n), (p), (r), (t), (v), and (x), wherein said DNA has a base sequence defined as

follows:

- 5 (b) a base sequence that hybridizes under stringent conditions with
a DNA having a base sequence complementary to a base
sequence consisting of base numbers 127 to 1908 of SEQ ID
NO: 5, and encodes a protein that has at least 50% of the
peptide-forming activity at 50°C and a pH of 8 of a protein
encoded by unmutated base numbers 127 to 1908 of SEQ ID
NO: 5,
- 10 (d) a base sequence that hybridizes under stringent conditions with
a DNA having a base sequence complementary to a base
sequence consisting of base numbers 121 to 1917 of SEQ ID
NO: 11, and encodes a protein that has at least 50% of the
peptide-forming activity at 50°C and a pH of 8 of a protein
encoded by unmutated base numbers 121 to 1917 of SEQ ID
15 NO: 11,
- 20 (f) a base sequence that hybridizes under stringent conditions with a
DNA having a base sequence complementary to a base
sequence consisting of base numbers 127 to 1935 of SEQ ID
NO: 17, and encodes a protein that has at least 50% of the
peptide-forming activity at 50°C and a pH of 8 of a protein
encoded by unmutated base numbers 127 to 1935 of SEQ ID
NO: 17,
- 25 (h) a base sequence that hybridizes under stringent conditions with
a DNA having a base sequence complementary to a base
sequence consisting of bases numbers 127 to 1995 of SEQ ID

- NO: 22, and encodes a protein that has at least 50% of the peptide-forming activity at 50°C and a pH of 8 of a protein encoded by unmutated base numbers 127 to 1995 of SEQ ID NO: 22,
- 5 (j) a base sequence that hybridizes under stringent conditions with a DNA having a base sequence complementary to a base sequence consisting of base numbers 104 to 1888 of SEQ ID NO: 24, and encodes a protein that has at least 50% of the peptide-forming activity at 50°C and a pH of 8 of a protein
- 10 encoded by unmutated base numbers 104 to 1888 of SEQ ID NO: 24,
- (l) a base sequence that hybridizes under stringent conditions with a DNA having a base sequence complementary to a base sequence consisting of base numbers 112 to 1992 of SEQ ID
- 15 NO: 26, and encodes a protein that has at least 50% of the peptide-forming activity at 50°C and a pH of 8 of a protein encoded by unmutated base numbers 112 to 1992 of SEQ ID NO: 26,
- (n) a base sequence that hybridizes under stringent conditions with
- 20 a DNA having a base sequence complementary to a base sequence consisting of base numbers 61 to 1908 of SEQ ID NO: 5, and encodes a protein containing a mature protein region and has at least 50% of the peptide-forming activity at 50°C and a pH of 8 of a protein encoded by unmutated base numbers 61
- 25 to 1908 of SEQ ID NO: 5,

- 5 (p) a base sequence that hybridizes under stringent conditions with
a DNA having a base sequence complementary to a base
sequence consisting of base numbers 61 to 1917 of SEQ ID NO:
11, and encodes a protein containing a mature protein region
and has at least 50% of the peptide-forming activity at 50°C and
a pH of 8 of a protein encoded by unmutated base numbers 61
to 1917 of SEQ ID NO: 11,
- 10 (r) a base sequence that hybridizes under stringent conditions with
a DNA having a base sequence complementary to a base
sequence consisting of base numbers 61 to 1935 of SEQ ID NO:
17, and encodes a protein containing a mature protein region
and has at least 50% of the peptide-forming activity at 50°C and
a pH of 8 of a protein encoded by unmutated base numbers 61
to 1935 of SEQ ID NO: 17,
- 15 (t) a base sequence that hybridizes under stringent conditions with a
DNA having a base sequence complementary to a base
sequence consisting of base numbers 61 to 1995 of SEQ ID NO:
22, and encodes a protein containing a mature protein region
and has at least 50% of the peptide-forming activity at 50°C and
20 a pH of 8 of a protein encoded by unmutated base numbers 61
to 1995 of SEQ ID NO: 22,
- 25 (v) a base sequence that hybridizes under stringent conditions with
a DNA having a base sequence complementary to a base
sequence consisting of base numbers 29 to 1888 of SEQ ID NO:
24, and encodes a protein containing a mature protein region

and has at least 50% of the peptide-forming activity at 50°C and a pH of 8 of a protein encoded by unmutated base numbers 29 to 1888 of SEQ ID NO: 24, or

(x) a base sequence that hybridizes under stringent conditions with a DNA having a base sequence complementary to a base sequence consisting of base numbers 61 to 1992 of SEQ ID NO: 26, and encodes a protein containing a mature protein region and has at least 50% of the peptide-forming activity at 50°C and a pH of 8 of a protein encoded by unmutated base numbers 61 to 1992 of SEQ ID NO: 26.

27. A recombinant DNA comprising the DNA according to Claim 26.

28. A transformed cell comprising the recombinant DNA according to Claim 26.

29. A method for producing a peptide-forming enzyme comprising: culturing the transformed cell according to Claim 28 in a medium for a time and under conditions suitable to produce the peptide-forming enzyme, and

accumulating the peptide-forming enzyme in the medium and/or transformed cell.

30. A method for producing a dipeptide comprising: culturing the transformed cell according to Claim 28 in a medium for a time and under conditions suitable to produce a peptide-forming enzyme in a culture, and

mixing the culture with a carboxy component and an amine

component to synthesize a dipeptide by enzymatic catalysis facilitated by a

peptide-forming enzyme encoded by said DNA.

31. The method for producing a dipeptide according to Claim 30,
wherein said cell is a microbe belonging to the genus *Sphingobacterium* that
has an ability to form the dipeptide from the carboxy component and the
5 amine component.

32. The method for producing a dipeptide according to Claim 31,
wherein said cell is separated from said culture.

33. The method for producing a dipeptide according to Claim 31,
wherein said cell is a treated microbial cell product of the microbe.

10 34. The DNA according to Claim 26, wherein stringent conditions are
conditions under which washing is carried out at 60°C at a salt concentration
equivalent to 1 × SSC and 0.1% SDS.

35. A recombinant DNA comprising the DNA according to Claim 34.

36. A transformed cell comprising the recombinant DNA according to
15 Claim 35.

37. A method for producing a peptide-forming enzyme comprising:
culturing the transformed cell according to Claim 36 in a medium for a
time and under conditions suitable to produce the peptide-forming enzyme,
and

20 accumulating the peptide-forming enzyme in the medium and/or
transformed cell.

38. A method for producing a dipeptide comprising:

culturing the transformed cell according to Claim 36 in a medium for a
time and under conditions suitable to produce a peptide-forming enzyme in a
25 culture, and

mixing the culture with a carboxy component and an amine component to synthesize a dipeptide by enzymatic catalysis facilitated by a peptide-forming enzyme encoded by said DNA.

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